#11/43

PATENT

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s)	Van Ommen, et al.	Examiner:	C. Wilder
Serial No.:	09/445,174	Group Art Unit:	1655
Filed:	April 24, 2000	Docket:	294-78
For:	DIAGNOSTIC TEST KIT FOR DETERMINING A PREDISPOSITION FOR BREAST AND OVARIAN CANCER, MATERIALS AND METHODS FOR SUCH DETERMINATION	Dated:	October 18, 2000

Assistant Commissioner for Patents
Washington, DC 20231

I hereby certify this correspondence is being deposited with the United States Postal Service as first class mail, postpaid in an envelope, addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231 on October 18, 2000

Dated: 10/18/00

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATION CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures mailed September 8, 2000, Applicants enclose herewith the following:

1.   Diskette containing a substitute Sequence Listing in computer-readable form, corrected as directed in the Notice;

2.   A substitute paper copy of the "Sequence Listing"; and

3. A copy of the Notice to Comply.

REMARKS

Applicants have amended the Sequence Listing to conform with the above-referenced Notice to Comply. Entry of the amended Sequence Listing into the specification of the application is respectfully requested.

The Notice to Comply dated September 8, 2000 indicates that the due date for a response to the Notice is the one-month shortened statutory period. This Response is filed within the second month after the September 8, 2000 communication. Accordingly, a Petition for a One Month Extension of Time and the appropriate fee are filed concurrently herewith.

The assignee is a small entity. Therefore, the reduced extension of time fee is being paid. A Declaration Claiming Small Entity is enclosed.
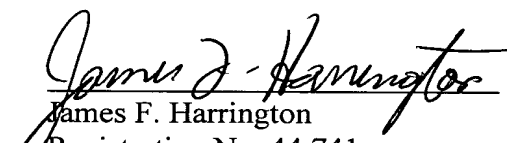
In compliance with the sequence rules as required under 37 C.F.R. §§1.821-1.825, Applicants have amended SEQ. ID NO.: 21 to delete reference to "n". The presence of "n" in the sequence listing was an error. Applicants provide herewith a computer readable form and a paper copy of the corrected Sequence Listing thereby satisfying the requirement under 37 C.F.R. §§1.821 *et seq.*

Under 37 C.F.R. 1.821(f), the Applicants' attorney hereby states that the contents of the computer readable form and the paper copy are the same. Under 37 C.F.R. §1.821(g), the

Applicants' attorney also states that the inclusion of this Sequence Listing does not include any new matter. Accordingly, it is respectfully requested that the Sequence Listing be entered into the application.

If the Examiner has any questions relating to this Amendment or to this application in general, it is respectfully requested that the Examiner contact the Applicants' undersigned attorney at the telephone number provided below.

Respectfully submitted,

James F. Harrington
Registration No. 44,741
Attorney for Applicants

HOFMANN & BARON, LLP
6900 Jericho Turnpike
Syosset, New York 11791
(516) 822-3550
JFH:jlw

121195_1.DOC

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXR.	
Debra Shoemaker	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXR. in charge of this application

Commissioner of Patents

1. The communication filed 7/13/2000 is not fully responsive to the Office communication mailed 6/13/2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

2. Any inquiry concerning this communication or earlier communications from the Exr. Should be directed to Cynthia Wilder whose telephone number is (703) 305-1680. The Exr. Can normally be reached on Monday-Thursday from 6:30-5:00 pm (Eastern Time).

If attempts to reach the Exr. by telephone are unsuccessful, the Exr.'s supervisor Gary Jones, can be reached at (703) 308-1152. The official fax number for group 1600 is (703) 308-4242, unofficial fax number for group 1600 is (703) 308-8724.

Any inquiry of a general nature or relating to the status of the application should be directed to the groups receptionist whose telephone number is (703) 308-0196.

Cynthia B. Wilder, PhD

Cynthia B. Wilder, PhD
September 5, 2000

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:_____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/445,774_

Source: _1635_

Date Processed by STIC: _7-26-00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker.

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: _09/445,174_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                  This may occur if your file was retrieved in a word processor after creating it.
                                  Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped" down to the next line.
                                  This may occur if your file was retrieved in a word processor after creating it.
                                  Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                  Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                  As per the rules, each n or Xaa can only represent a single residue.
                                  Please present the maximum number of each residue having variable length and
                                  indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                  sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                  to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
                                  sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                                  (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                  This sequence is intentionally skipped

                                  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                                  <400> sequence id number
                                  000

10 ✓   Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                  Please explain source of genetic material in <220> to <223> section.
                                  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                                  file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                  Instead, please use "File Manager" or any other means to copy file to floppy disk.

```
           RAW SEQUENCE LISTING               DATE: 07/26/2000
           PATENT APPLICATION:  US/09/445,174  TIME: 10:17:06

           Input Set : A:\115541_1.txt
           Output Set: N:\CRF3\07262000\I445174.raw
```

```
 1 <110> APPLICANT: van Ommen, Garrit J.B.
 2         Petrij-Bosch, Anne
 3         Bakker, Egbert
 4         Devilee, Peter
 7 <120> TITLE OF INVENTION: A diagnostic test kit for determining a predisposition
 8         for breast and ovarian cancer, materials and methods
 9         for such determination
11 <130> FILE REFERENCE: P22163CA00
13 <140> CURRENT APPLICATION NUMBER: US 09/445,174
14 <141> CURRENT FILING DATE: 2000-04-24
16 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00325
17 <151> PRIOR FILING DATE: 1998-06-03
19 <150> PRIOR APPLICATION NUMBER: EP 97201700.8
20 <151> PRIOR FILING DATE: 1997-06-04
22 <160> NUMBER OF SEQ ID NOS: 23
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
33         for D17S1322
35 <400> SEQUENCE: 1
36 ctagcctggg caacaaacga                                    20
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
46         for D17S1322
48 <400> SEQUENCE: 2
49 gcaggaagca ggaatggaac                                    20
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 21
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
59         for D17S855
61 <400> SEQUENCE: 3
62 ggatggcctt ttagaaagtg g                                  21
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 20
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
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```
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
72        for D17S855
74 <400> SEQUENCE: 4
75 acacagactt gtcctactgc                                    20
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
85        for D17S1323
87 <400> SEQUENCE: 5
88 taggagatgg attattggtg                                    20
91 <210> SEQ ID NO: 6
92 <211> LENGTH: 20
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
98        for D17S1323
100 <400> SEQUENCE: 6
101 aagcaacttt gcaatgagtg                                   20
104 <210> SEQ ID NO: 7
105 <211> LENGTH: 22
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
111        for first PCR
113 <400> SEQUENCE: 7
114 tcacagtgca gtgaattgga ag                                22
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 24
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
124        for first PCR
126 <400> SEQUENCE: 8
127 gtagccagga cagtagaagg actg                              24
130 <210> SEQ ID NO: 9
131 <211> LENGTH: 22
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
137        for second PCR
139 <400> SEQUENCE: 9
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000
TIME: 10:17:06

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\I445174.raw

```
140 gaagaaagag gaacgggctt gg                                          22
143 <210> SEQ ID NO: 10
144 <211> LENGTH: 21
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
150      for second PCR
152 <400> SEQUENCE: 10
153 ggccactttg taagctcatt c                                           21
156 <210> SEQ ID NO: 11
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
164 <400> SEQUENCE: 11
165 aaccaccaag gtccaaagc                                              19
168 <210> SEQ ID NO: 12
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
176 <400> SEQUENCE: 12
177 gtagccagga cagtagaagg actg                                        24
180 <210> SEQ ID NO: 13
181 <211> LENGTH: 20
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
188 <400> SEQUENCE: 13
189 tacgtgggtt caactgaagc                                             20
192 <210> SEQ ID NO: 14
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
200 <400> SEQUENCE: 14
201 tcccattgag aggtcttgct                                             20
204 <210> SEQ ID NO: 15
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
212 <400> SEQUENCE: 15
```

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\I445174.raw

```
213 actgtgctac tcaagcacca                                      20
216 <210> SEQ ID NO: 16
217 <211> LENGTH: 24
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
224 <400> SEQUENCE: 16
225 gaaaaaaaag tacaaccaaa tgcc                                 24
228 <210> SEQ ID NO: 17
229 <211> LENGTH: 24
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
236 <400> SEQUENCE: 17
237 agcccacttc attagtactg gaac                                 24
240 <210> SEQ ID NO: 18
241 <211> LENGTH: 24
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
248 <400> SEQUENCE: 18
249 taccctataa gccagaatcc agaa                                 24
252 <210> SEQ ID NO: 19
253 <211> LENGTH: 21
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
260 <400> SEQUENCE: 19
261 ggccactttg taagctcatt c                                    21
264 <210> SEQ ID NO: 20
265 <211> LENGTH: 720
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <220> FEATURE:
270 <223> OTHER INFORMATION: /note="Exon 22 of BRCA1 and its flanking intron
271       sequences, pos. 79441-80160"
273 <400> SEQUENCE: 20
274 agaggtcttg ctataagcct tcatccggag agtgtagggt agagggcctg ggttaagtat 60
275 gcagattact gcagtgattt tacatctaaa tgtccatttt agatcaactg gaatggatgg 120
276 tacagctgtg tggtgcttct gtggtgaagg agctttcatc attcaccctt ggcacagtaa 180
277 gtattgggtg ccctgtcaga gagggaggac acaatattct ctcctgtgag caagactggc 240
278 acctgtcagt ccctatggat gcccctactg tagcctcaga agtcttctct gcccacatac 300
279 ctgtgccaaa agactccatc tgtaagggat gggtaaggat ttgagaactg cacatattaa 360
280 atatactgag ggaagacttt ttccctctaa ctcttttccc catatgtccc tcccctcct 420
281 ctctgtgact gccccagcat actgtgtttc aacaaatcat caagaaatga tgggctggag 480
```

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\I445174.raw

```
282 gctgggcatg gtggctcatg tctgtaatcc cagcactttg ggaggccgag gcaggtggat 540
283 cacttgtcag gagtttgaga ccagcctggc caacatggtg aaaccccatc tgtactaaaa 600
284 aaaaaaaaac aaaaagtagc caggcctggt ggagcatgcc tgtaatgcca gctatttggg 660
285 aagttgaggt gtgagcatcg cttgaacgtg ggaggcagag gttgcagtga gccaagattg 720
288 <210> SEQ ID NO: 21
289 <211> LENGTH: 180
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <223> OTHER INFORMATION: /note="Intronic region flanking exon 12, pos.
295       44423 - 44600"
297 <400> SEQUENCE: 21
W--> 298 cctgtaatcc cagcactttg ggaggccgag gcgggaggat catgtgangt caggagatcc 60
299 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagctg 120
300 ggcatggtgg cgggcgcctg taatcccagc tactcaggag gctgaagcag aagaatggct 180
303 <210> SEQ ID NO: 22
304 <211> LENGTH: 180
305 <212> TYPE: DNA
306 <213> ORGANISM: Homo sapiens
308 <220> FEATURE:
309 <223> OTHER INFORMATION: /note="Intronic region flanking exon 13, pos.
310       48256 - 48436"
312 <400> SEQUENCE: 22
313 cctgtaaccc cagcactttg ggaggccaag gcaggcgaat cacctgaggt cgggagctcg 60
314 agaccagcct gaccaacatg gagaaaccac atctctacta aaactacaaa aaattagccg 120
315 ggcgtggtgg cacatgcctg taatcccagc tacttgggag ctacggtgcc tggcctagtt 180
318 <210> SEQ ID NO: 23
319 <211> LENGTH: 60
320 <212> TYPE: DNA
321 <213> ORGANISM: Homo sapiens
323 <220> FEATURE:
324 <223> OTHER INFORMATION: /note="Deletion-function fragment"
326 <400> SEQUENCE: 23
327 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagccg 60
```

Mandatory features missing <221> <222> <223>. Explain location of n's and residues they represent.

See #10 on Error Summary Sheet.

L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21